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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/833,117

DATE: 05/02/2001

TIME: 12:21:03

Input Set : A:\PF543SL.txt

Output Set: N:\CRF3\05022001\I833117.raw

3 <110> APPLICANT: Rosen, Craig A.
4 Sadeghi, Homa
5 Prior, Christopher P.
6 Turner, Andrew J.
8 <120> TITLE OF INVENTION: Albumin Fusion Proteins
10 <130> FILE REFERENCE: PF543
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/833,117
13 <141> CURRENT FILING DATE: 2001-04-12
15 <150> PRIOR APPLICATION NUMBER: 60/229,358
16 <151> PRIOR FILING DATE: 2000-04-12
18 <150> PRIOR APPLICATION NUMBER: 60/256,931
19 <151> PRIOR FILING DATE: 2000-12-21
21 <150> PRIOR APPLICATION NUMBER: 60/199,384
22 <151> PRIOR FILING DATE: 2000-04-25
24 <160> NUMBER OF SEQ ID NOS: 36
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 23
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <221> NAME/KEY: primer bind
35 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
37 <400> SEQUENCE: 1
38 cccaagaatt ccttatcca ggc 23
41 <210> SEQ ID NO: 2
42 <211> LENGTH: 33
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <221> NAME/KEY: primer_bind
48 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
50 <400> SEQUENCE: 2
51 qqqaagctta qaaqcacag gatacctcca cag 33
54 <210> SEQ ID NO: 3
55 <211> LENGTH: 16
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <221> NAME/KEY: misc_structure
61 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
62 with non-cohesive ends.
64 <400> SEQUENCE: 3
65 gataaagatt cccaac 16
68 <210> SEQ ID NO: 4
69 <211> LENGTH: 17
70 <212> TYPE: DNA

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71 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
73 <221> NAME/KEY: misc_structure
74 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
75 with non-cohesive ends.
76 <400> SEQUENCE: 4
77 aattgttggg aatcttt 17
78 <210> SEQ ID NO: 5
79 <211> LENGTH: 17
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <221> NAME/KEY: misc_structure
84 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
85 with non-cohesive ends.
86 <400> SEQUENCE: 5
87 ttagcttat tcccaac 17
88 <210> SEQ ID NO: 6
89 <211> LENGTH: 18
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <221> NAME/KEY: misc_structure
94 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
95 with non-cohesive ends.
96 <400> SEQUENCE: 6
97 aattgttggg aataagcc 18
98 <210> SEQ ID NO: 7
99 <211> LENGTH: 24
100 <212> TYPE: PRT
101 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <221> NAME/KEY: SITE
104 <222> LOCATION: 1)..(19)
105 <223> OTHER INFORMATION: invertase leader sequence
106 <220> FEATURE:
107 <221> NAME/KEY: SITE
108 <222> LOCATION: 20)..(24)
109 <223> OTHER INFORMATION: first 5 amino acids of mature human serum albumin
110 <400> SEQUENCE: 7
111 Met Leu Leu Gln Ala Phe Leu Phe Leu Ala Gly Phe Ala Ala Lys
112 1 5 10 15
113 Ile Ser Ala Asp Ala His Lys Ser
114 20
115 <210> SEQ ID NO: 8
116 <211> LENGTH: 21
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:

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139 <221> NAME/KEY: misc structure
140 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
141     fragments with non-cohesive ends.
143 <400> SEQUENCE: 8
144 qagatgcaca cctgagtgaq g                               21
147 <210> SEQ ID NO: 9
148 <211> LENGTH: 27
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <221> NAME/KEY: misc_structure
154 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
155     fragments with non-cohesive ends.
157 <400> SEQUENCE: 9
158 gatcctgttg cttcgatqca cacaaqa                               27
161 <210> SEQ ID NO: 10
162 <211> LENGTH: 24
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <221> NAME/KEY: misc_structure
168 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
169     fragments with non-cohesive ends.
171 <400> SEQUENCE: 10
172 ctcttqtgtg catcgaagcc acag                               24
175 <210> SEQ ID NO: 11
176 <211> LENGTH: 30
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <221> NAME/KEY: misc_structure
182 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
183     fragments with non-cohesive ends.
185 <400> SEQUENCE: 11
186 tgttqqaagag cctcagaatt tattcccaac                       30
189 <210> SEQ ID NO: 12
190 <211> LENGTH: 31
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <221> NAME/KEY: misc_structure
196 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
197     fragments with non-cohesive ends.
199 <400> SEQUENCE: 12
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203 <210> SEQ ID NO: 13
204 <211> LENGTH: 47
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence

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208 <220> FEATURE:
209 <221> NAME/KEY: misc_structure
210 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
211     fragments with non-cohesive ends.
213 <400> SEQUENCE: 13
214 ttaggcttag gtgcggtgq atccgcggtt ggtggaictt tcccaac      47
217 <210> SEQ ID NO: 14
218 <211> LENGTH: 48
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <221> NAME/KEY: misc_structure
224 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
225     fragments with non-cohesive ends.
227 <400> SEQUENCE: 14
228 aattgttggg aaagatccac caccgcgga tccacgcga cctaaagg      48
231 <210> SEQ ID NO: 15
232 <211> LENGTH: 62
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <221> NAME/KEY: misc_structure
238 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
239     fragments with non-cohesive ends.
241 <400> SEQUENCE: 15
242 ttaggcttag gcggtggtg atctagtgg ggcggaatctg gtgcggtgq atccttccca 60
243 ac      62
246 <210> SEQ ID NO: 16
247 <211> LENGTH: 63
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <221> NAME/KEY: misc_structure
253 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
254     fragments with non-cohesive ends.
256 <400> SEQUENCE: 16
257 aattgttggg aaagatccac cccacgcga tccgcgcga caagatccac caccgcctaa 60
258 gcc      63
261 <210> SEQ ID NO: 17
262 <211> LENGTH: 1782
263 <212> TYPE: DNA
264 <213> ORGANISM: Homo sapiens
266 <220> FEATURE:
267 <221> NAME/KEY: CDS
268 <222> LOCATION: (1)..(1755)
271 <400> SEQUENCE: 17
272 gat gca cac aag agt gaq gtt gct cat cgg ttt aaa gat ttg gga gaa      48
273 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
274   1           5           10           15

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```

276 qaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag 96
277 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
278                20                25                30
280 cag tgt cca ttt qaa gat cat gta aaa tta gtg aat qaa gta act qaa 144
281 Gln Cys Pro Phe Gln Asp His Val Lys Leu Val Asn Glu Val Thr Glu
282                35                40                45
284 ttt gca aaa aca tgt qtt gct qat qag tca gct qaa aat tgt qac aaa 192
285 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
286                50                55                60
288 tca ctt cat acc ctt ttt qga gac aaa tta tgc aca gtt qca act ctt 240
289 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
290        65                70                75                80
292 cgt qaa acc tat qgt qaa atg gct qac tgc tgt qca aaa caa qaa cct 288
293 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
294                85                90                95
296 qag aqa aat qaa tgc ttc ttg caa cac aaa gat qac aac cca aac ctc 336
297 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
298                100                105                110
300 ccc cga ttg gtg aga cca qag qtt gat gtg atg tgc act gct ttt cat 384
301 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
302                115                120                125
304 qac aat qaa qag aca ttt ttg aaa tac tta tat qaa att gcc aqa 432
305 Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
306                130                135                140
308 aqa cat cct tac ttt tat gcc ccg qaa ctc ctt ttc ttt gct aaa agg 480
309 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
310        145                150                155                160
312 tat aaa gct gct ttt aca qaa tgt tgc caa gct gct qat aaa gct gcc 528
313 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
314                165                170                175
316 tgc ctg ttg cca aaq ctc gat qaa ctt ccg gat qaa qgg aag gct tgc 576
317 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
318                180                185                190
320 tct gcc aaa cag aqa ctc aaa tgt gcc agt ctc caa aaa ttt qga qaa 624
321 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
322                195                200                205
324 aqa gct ttc aaa qca tgg qca gtg gct cgc ctg agc cag aqa ttt ccc 672
325 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
326        210                215                220
328 aaa gct qag ttt qca qaa qtt tcc aaq tta gtg aca gat ctt acc aaa 720
329 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
330        225                230                235                240
332 gtc cac acg qaa tgc tgc cat gga gat ctg ctt qaa tgt gct gat gac 768
333 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
334                245                250                255
336 aag gcg qac ctt gcc aag tat atc tgt qaa aat cag gat tgc atc tcc 816
337 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
338                260                265                270
340 agt aaa ctg aag qaa tgc tgt qaa aaa cct ctg ttg qaa aaa tcc cac 864

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/833,117

DATE: 05/02/2001

TIME: 12:21:04

Input Set : A:\PF543SL.txt

Output Set : N:\CRF3\05022001\I833117.raw

L:12 M:270 C: Current Application Number differs. Replaced Current Application Number
L:710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:799 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:888 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33